

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: November 30, 2002, 12:02:18 ; Search time 16.7346 seconds

(without alignments)
2282.679 Million cell updates/sec

File: US-10-054-680-2

Sequence: 1 MAMLRQPLRSALFLHGLVT.....LMLLYLFLATLEANCYIKGF 921

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database: SwissProt.40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	4686	97.7	927	1	NAC3_RAT
2	3447.5	71.9	970	1	NAC1_CANFA
3	3442.5	71.8	970	1	NAC1_FELCA
4	3439.5	71.7	973	1	NAC1_HUMAN
5	3432.5	71.6	970	1	NAC1_CANVO
6	3428	71.5	971	1	NAC1_RAT
7	3425.5	71.4	970	1	NAC1_BOVIN
8	3405.5	71.0	970	1	NAC1_MOUSE
9	3373.5	70.3	921	1	NAC2_HUMAN
10	3357	70.0	921	1	NAC2_RAT
11	3093	64.5	595	1	NAC3_HUMAN
12	306.5	6.4	1216	1	NKX1_BOVIN
13	303.5	6.3	1181	1	NKX1_RAT
14	293	6.1	1099	1	NKX1_HUMAN
15	266	5.5	645	1	NKX3_MOUSE
16	262.5	5.5	624	1	NKX3_RAT
17	258.5	5.4	644	1	NKX3_HUMAN
18	251	5.2	663	1	NKX1_CHICK
19	239.5	5.0	661	1	NKX2_HUMAN
20	231.5	4.8	856	1	NCKX2_MOUSE
21	227	4.7	670	1	NKX2_RAT
22	216.5	4.5	651	1	NKX2_CHICK
23	147	3.1	590	1	YKTA_CAEL
24	143.5	3.0	325	1	YRBG_ECOLI
25	142.5	3.0	1807	1	YRBG_ECOLI
26	142	3.0	302	1	YRBG_ECOLI
27	141.5	2.9	572	1	YRBG_ECOLI
28	138.5	2.7	664	1	YRBG_ECOLI
29	128.5	2.7	4655	1	LRP2_HUMAN
30	127	2.6	1822	1	LRP2_HUMAN
31	125	2.6	700	1	TRDN_CANFA
32	120	2.5	1828	1	MAP2_MOUSE
33	119.5	2.5	1564	1	MRP2_RABIT

34	118	2.5	803	1	RIR1_CRYPV
35	115.5	2.4	1805	1	NKX3_RAT
36	115	2.4	548	1	CH60_EHRE
37	114	2.4	1036	1	YAN2_SCHO
38	114	2.4	1468	1	RPOB_AOUAE
39	113.5	2.4	548	1	CH60_EHRE
40	113.5	2.4	661	1	Y102_MYCTU
41	113.5	2.4	1332	1	SPT7_YEAST
42	113.5	2.4	1612	1	ATC4_YEAST
43	112	2.3	853	1	YCG1_YEAST
44	112	2.3	1112	1	RA13_SCHO
45	111.5	2.3	853	1	VMTH_LAMBD

ALIGNMENTS

RESULT 1	ID	NAME	STANDARD	PRT	927 AA
NAC3_RAT	AC	P70549			
DT	01-NOV-1997	(Rel. 35, Created)			
DT	01-NOV-1997	(Rel. 35, Last sequence update)			
DT	15-JUN-2002	(Rel. 41, Last annotation update)			
DE	Sodium/calcium exchanger 3 precursor (Na(+)/Ca(2+)-exchange protein 3).				
GN	SLC8A3 OR NCX3.				
OS	Rattus norvegicus (Rat).				
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.				
OX	NCBI_TaxID=10116;				
RM	[1]				
RP	SEQUENCE FROM N.A.				
RC	STRAIN-Sprague-Dawley; TISSUE-Brain;				
RX	MEDLINE=96394663; PubMed=8798769;				
RA	Nicola D.A., Quednau B.D., Qui Z., Xia Y.-R., Lusis A.J.,				
RA	Philipson K.D.;				
RT	"Cloning of a third mammalian Na(+)-Ca(2+) exchanger, NCX3.,"				
RL	J. Biol. Chem. 271:24914-24921(1996).				
CC	-1- FUNCTION: RAPIDLY TRANSPORTS CA2+ DURING EXCITATION-CONTRACTION				
CC	COUPLING. CA(2+) IS EXTRUDED FROM THE CELL DURING RELAXATION				
CC	SO AS TO PREVENT OVERLOADING OF INTRACELLULAR STORES.				
CC	-1- ENZYME REGULATION: BY INTRACELLULAR CALCIUM IONS.				
CC	-1- SUBCELLULAR LOCATION: Integral membrane protein.				
CC	-1- TISSUE SPECIFICITY: EXPRESSION RESTRICTED TO BRAIN AND SKELETAL				
CC	MUSCLE.				
CC	-----				
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration				
CC	between the Swiss Institute of Bioinformatics and the EMBL outstation -				
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CC	entities requires a license agreement (see http://www.isb-sib.ch/announce/				
CC	or send an email to license@sib-sib.ch).				
CC	-----				
CC	EMBL: U53420; AAC52817.1; -				
CC	InterPro: IPR003644; Calx_beta.				
CC	InterPro: IPR004837; NaCa_Exmemb.				
CC	InterPro: IPR004836; NaCa_Ex.				
CC	Pfam: PF01699; Na_Ca_Ex: 2.				
CC	Pfam: PF03160; Calx_beta: 2.				
CC	PRINTS: PR01259; NACAEXCHNGR.				
CC	SMART: SM00237; Calx_beta: 2.				
CC	TIGRFAMs: TIGR00845; caca; 1.				
CC	Transmembrane: Glycoprotein; Phosphorylation; Signal;				
CC	Transmembrane: Glycoprotein; Phosphorylation; Signal;				
CC	Calmodulin-binding; Repeat.				
CC	SIGNAL				
CC	1				
CC	30				
CC	POTENTIAL.				
CC	SODIUM/CALCIUM EXCHANGER 3.				
CC	EXTRACELLULAR (POTENTIAL).				
CC	POTENTIAL.				
CC	TRANSMEM				
CC	95				
CC	147				
CC	CYTOPLASMIC (POTENTIAL).				
CC	POTENTIAL.				
CC	TRANSMEM				
CC	148				
CC	168				

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FT DOMAIN 169 169 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 170 190 POTENTIAL.
FT DOMAIN 191 202 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 203 223 POTENTIAL.
FT DOMAIN 224 230 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 231 251 POTENTIAL.
FT DOMAIN 252 276 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 277 277 POTENTIAL.
FT TRANSMEM 278 278 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 279 279 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 280 282 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 283 283 POTENTIAL.
FT TRANSMEM 284 284 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 285 285 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 286 286 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 287 287 POTENTIAL.
FT TRANSMEM 288 288 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 289 289 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 290 290 POTENTIAL.
FT TRANSMEM 291 291 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 292 292 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 293 293 CALMODULIN-BINDING (BY SIMILARITY).
FT TRANSMEM 294 294 ALPHA-1.
FT TRANSMEM 295 295 BETA-1.
FT TRANSMEM 296 296 BETA-2.
FT TRANSMEM 297 297 POLY-GLU.
FT TRANSMEM 298 298 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT TRANSMEM 299 299 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT TRANSMEM 300 300 SEQUENCE 927 AA: 103162 MW: 103162 MB: EAB35F9620DBE69E CRC64:

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Query Match 97.7%; Score 4686; DB 1; Length 927;
Best Local Similarity 96.8%; Pred. No. 1.6e-300;
Matches 897; Conservative 14; Mismatches 10; Indels 6; Gaps 1;

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QY 1 MAULRLOPLSAPLHGLVFLVFLNGLRAGSGSDPSTGNNESGSSDCKEVL 60
DB 1 MAULRLOPLSAPLHGLVFLVFLNGLRAGSDPSTGNNESGSSDCKEVL 60
QY 61 PIWYPPNSLGRKIRIYVYFVALIYVGLVSIADRFNASIEVITSOEREVTKRNGE 120
DB 61 PIWYPPNSLGRKIRIYVYFVALIYVGLVSIADRFNASIEVITSOEREVTKRNGE 120
QY 121 TSTTTIRVWNETVSNLTMLAGSSAPRILLSLIEVCGHGFIADLGRSTVGSAAFMFI 180
DB 121 TSTTTIRVWNETVSNLTMLAGSSAPRILLSLIEVCGHGFIADLGRSTVGSAAFMFI 180
QY 181 IIGICVIVIDGERTKIKHLRVFETPAASIFAYIMLYMLAVFSPVQVWEGLLTF 240
DB 181 IIGICVIVIDGERTKIKHLRVFETPAASIFAYIMLYMLAVFSPVQVWEGLLTF 240
QY 241 FVYCVLLAWADRRLLEYKYMHRKYRTDKHGGIIEGSDHPKGIEMGKMMNSHFLDGN 300
DB 241 FVYCVLLAWADRRLLEYKYMHRKYRTDKHGGIIEGSDHPKGIEMGKMMNSHFLDGN 300
QY 301 LVPLEGEVDESREMRIRIKDKOKHPEKDQDQVEMANYALSHOQKRAATRIQAT 360
DB 301 LVPLEGEVDESREMRIRIKDKOKHPEKDQDQVEMANYALSHOQKRAATRIQAT 360
QY 361 LIPLEGVEVESREMRIRIKDKOKHPEKDQDQVEMANYALSHOQKRAATRIQAT 420
DB 361 LIPLEGVEVESREMRIRIKDKOKHPEKDQDQVEMANYALSHOQKRAATRIQAT 420
QY 421 KGGDMKTMVVDYKTEDGSANAGADYEFTGTVVLKPGETOKEFSVGIIDDDFEEDHF 480
DB 421 KGGDMKTMVVDYKTEDGSANAGADYEFTGTVVLKPGETOKEFSVGIIDDDFEEDHF 480
QY 481 FVRLSNRRIEEOPEBSMPAIFNSLPLPRAVLAAPCVATVTIIDDHAGIFFECDTH 540
DB 481 FVRLSNRRIEEOPEBSMPAIFNSLPLPRAVLAAPCVATVTIIDDHAGIFFECDTH 540
QY 541 VSSSIGMEVKVLRTSARGATVIVPFTVGTAKGGGEDEEDYIGLEFNDFTVKIRV 600
DB 541 VSSSIGMEVKVLRTSARGATVIVPFTVGTAKGGGEDEEDYIGLEFNDFTVKIRV 600

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QY 601 KIVDEEYEROEENFIALGEPKMERGIS-----DYTRKLTMEBEAKRIAEKGPVL 654
DB 601 KIVDEEYEROEENFIALGEPKMERGISALLSPVETDRKLTMEBEAKRIAEKGPVL 660
QY 655 GEHPRKEVIEEERKTYVDKIKTKTNLALVYQTHSWBDOFEATVYAAAGDEDESG 714
DB 655 GEHPRKEVIEEERKTYVDKIKTKTNLALVYQTHSWBDOFEATVYAAAGDEDESG 720
QY 715 EERLPCFQVYVHFLTFVFKVLEFACVPPEYCHGACFAVSILIIOMLTALIGDLASHFG 774
DB 721 EERLPCFQVYVHFLTFVFKVLEFACVPPEYCHGACFAVSILIIOMLTALIGDLASHFG 780
QY 775 CTIGLDSYAVVFAVFGSVPTFASKAALODYADASIGNVTSNANVFLIGIGLAM 834
DB 781 CTIGLDSYAVVFAVFGSVPTFASKAALODYADASIGNVTSNANVFLIGIGLAM 840
QY 835 SVATYMALOGEHEVHVSAGLAFSVLTFIFAVCSIVLLYRRRPHLGGELGPRCKLA 894
DB 841 SVATYMALOGEHEVHVSAGLAFSVLTFIFAVCSIVLLYRRRPHLGGELGPRCKLA 900
QY 895 TTVLFSVLMILYLFATLEAVCYIKGF 921
DB 901 TTVLFSVLMILYLFATLEAVCYIKGF 927

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RESULT 2
ID NACL_CANFA STANDARD; PRT; 970 AA.
AC P23685;
DT 01-NOV-1991 (Rel. 20, Created)
DT 01-NOV-1991 (Rel. 20, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Sodium/calcium exchanger 1 precursor (Na(+)/Ca(2+)-exchange protein
  1).
GN SLC8A1.
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX NCBI_TaxID=9615;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Heart;
RX MEDLINE=91047958; PubMed=1700476;
RA Nicoll D.A., Longoni S., Philipson K.D.;
RT "Molecular cloning and functional expression of the cardiac
  sarcolemmal Na(+)-Ca2+ exchanger.";
RL Science 250:562-565(1990).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Heart;
RX MEDLINE=92152737; PubMed=1785844;
RA Nicoll D.A., Philipson K.D.;
RT "Molecular studies of the cardiac sarcolemmal sodium-calcium
  exchanger.";
RL Ann. N.Y. Acad. Sci. 639:181-188(1991).
CC - FUNCTION: RAPIDLY TRANSPORTS CA2+ DURING EXCITATION-CONTRACTION
  COUPLING. CA(2+) IS EXTRUDED FROM THE CELL DURING RELAXATION
  SO AS TO PREVENT OVERLOADING OF INTRACELLULAR STORES.
CC - ENZYME REGULATION: BY ATP.
CC - SUBCELLULAR LOCATION: Integral membrane protein. Plasma membrane.
CC - TISSUE SPECIFICITY: CARDIAC SARCOLEMA.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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DR EMBL: M57523; AAA62766.1; -
DR PIR: A36417; A36417.
DR InterPro: IPR003644; Calx_beta.

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RX MEDLINE-97269065; PubMed-9111065;
 RA Barnes K.V., Cheng G., Dawson M.M., Menick D.R.;
 RT Cloning of cardiac, kidney, and brain promoters of the feline nck1
 gene.";
 RL J. Biol. Chem. 272:11510-11517(1997).
 CC -1- FUNCTION: RAPIDLY TRANSPORTS CA2+ DURING EXCITATION-CONTRACTION
 COUPLING. CA(2+) IS EXTRUDED FROM THE CELL DURING RELAXATION
 CC SO AS TO PREVENT OVERLOADING OF INTRACELLULAR STORES.
 CC -1- ENZYME REGULATION: BY ATP.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Plasma membrane.
 CC -1- TISSUE SPECIFICITY: CARDIAC SARCOLEMA.
 CC -----
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 CC -----
 DR EMBL: L35846; AAB41941.1; -
 DR EMBL: U67075; AAB40148.1; -
 DR InterPro: IPR003644; Calx_beta.
 DR InterPro: IPR004837; NaCa_Extm.
 DR Pfam: PF01699; Na_Ca_Ext; 2.
 DR Pfam: PF03160; Calx_beta; 2.
 DR PRINTS: PRO1259; NACAEXCHNGR.
 DR SMART: SM00237; Calx_beta; 2.
 DR TIGR: TIGR00845; caca; 1.
 DR Transport: Sodium transport;
 KW Transmembrane; Glycoprotein; Phosphorylation; Signal;
 KW Calmodulin-binding; Repeat.
 FT SIGNAL 1 32
 FT CHAIN 33 970
 FT DOMAIN 33 71
 FT TRANSMEM 72 93
 FT DOMAIN 94 133
 FT TRANSMEM 134 155
 FT DOMAIN 156 167
 FT TRANSMEM 168 188
 FT DOMAIN 189 199
 FT TRANSMEM 200 222
 FT DOMAIN 223 225
 FT TRANSMEM 226 249
 FT DOMAIN 250 269
 FT TRANSMEM 270 770
 FT DOMAIN 790 796
 FT TRANSMEM 797 819
 FT DOMAIN 820 821
 FT TRANSMEM 822 840
 FT DOMAIN 841 871
 FT TRANSMEM 872 892
 FT DOMAIN 893 903
 FT TRANSMEM 904 924
 FT DOMAIN 925 941
 FT TRANSMEM 942 958
 FT DOMAIN 959 970
 FT TRANSMEM 251 270
 FT REPEAT 138 178
 FT REPEAT 407 478
 FT REPEAT 539 609
 FT REPEAT 839 875
 FT DOMAIN 236 239
 FT DOMAIN 689 692
 FT DOMAIN 756 760
 FT MOD_RES 389 389
 FT CARBOHYD 41 41
 FT CARBOHYD 157 157
 FT CONFLICT 21 21
 FT CONFLICT 113 113
 FT SEQUENCE 970 AA: 108004 MW: 2402602DE3504057 CAC64:

Query Match 71.8%; Score 3442.5; DB 1: Length 970;
 Best Local Similarity 69.3%; Pred. No. 1.1e-218;
 Matches 678; Conservative 108; Mismatches 67; Gaps 12;

QY 1 MAMLRLOPLTSANLHFGVTFV-LFLNGLRAREKSGGDVPSIQNNES--CSGSSCKRG 57
 DB 1 MAMLRISPFSVGFH--LAFVPLRLSHVDL--SADTMEDEGETEBCGSIYCKKG 55
 QY 58 VILPIWPNPSLGDRIARIYVFAVLIYWFELGVSIIADRFMAISVITSOEREVTKRP 117
 DB 56 VILPIWPNPSLGDRIARIYVFAVLIYWFELGVSIIADRFMAISVITSOEREVTKRP 115
 QY 118 NGESTTTRWNEVTSNLTALSSAPETILSLIEVCGHGFIACDLGPSTIVGSAAN 177
 DB 116 NGESTTTRWNEVTSNLTALSSAPETILSLIEVCGHGFIACDLGPSTIVGSAAN 175
 QY 178 MFIIDICVYVPDGEFRKIKHLRVEFTIAMSIFAYIMLYMLAFAFGVYVWGSLT 237
 DB 176 MFIIDICVYVPDGEFRKIKHLRVEFTIAMSIFAYIMLYMLAFAFGVYVWGSLT 235
 QY 238 LFFPVCVLLAWADRRLLFFKYMHKKRTDKRGIIETEGDHPKG---IEMDGKMMNS 294
 DB 236 FFFPVCVFWAWADRRLLFFKYMKRGRMIIIEGDRPSSKTEIEMDGKMMNS 295
 QY 295 H--FLDGLNVLPEKGVV---ESRREMIIRILKDIKQHPKEDLDQVEMANYVALSHQ 347
 DB 296 HVDNPLDGLV-LVEDRPDDDEARREMARILKELKQHPKEDLDQVEMANYVALSHQ 354
 QY 348 OKSRAFYRQATQMTMGAGIILKKHAAEQAKSSSEVHTDPE--DFISKVFEDECSTQ 406
 DB 355 OKSRAFYRQATQMTMGAGIILKKHAAEQAKSSSEVHTDPE--DFISKVFEDECSTQ 414
 QY 407 CLENGCAVLLTVVRKGDMSKTYVDYKTEDGSANAGADYEFTGTVVLKPGTEKFSV 466
 DB 415 CLENGCAVLLTVVRKGDMSKTYVDYKTEDGSANAGADYEFTGTVVLKPGTEKFSV 474
 QY 467 GIIDDDIIEDEHEFYRLSNVRIEEOPEGMPALFNSLPLRAVLASPCVATVITLD 526
 DB 475 GIIDDDIIEDEHEFYRLSNVRIEEOPEGMPALFNSLPLRAVLASPCVATVITLD 531
 QY 527 DHAGITFPGDTHVSESTGVMEVKYLRISGANGTYIVPRYEGTAKSGGEFETGYE 586
 DB 532 DHAGITFPGDTHVSESTGVMEVKYLRISGANGTYIVPRYEGTAKSGGEFETGYE 591
 QY 587 LEEKNDYKTIIRKIVDEEYERQDNFTALGEPRMWERG----- 627
 DB 592 LEEKNDYKTIIRKIVDEEYERQDNFTALGEPRMWERG----- 627
 QY 628 -----ISDYTRK--LTMEBEAKRIAMGRPVJGEHKLVEY 662
 DB 652 LYGQPVFRVYHAREHPISTVITIAEEDCAKOPLTSEKEEBERIAMGRPIIGEHKLEV 711
 QY 663 IIESEYEPKTYVTKLTKTNLALVGTSHWRDPMFAIVSAAGDEDESGEERLPSGF 722
 DB 712 IIESEYEPKTYVTKLTKTNLALVGTSHWRDPMFAIVSAAGDEDESGEERLPSGF 771
 QY 723 DYVMEHLTFWKVLFACVPTXCHMACFAVSILITIGMTALISDGLASHFGCTIGLKS 782
 DB 772 DYVMEHLTFWKVLFACVPTXCHMACFAVSILITIGMTALISDGLASHFGCTIGLKS 831
 QY 783 VTAIVFVAGTSVPDTFASKAALADVYIADASIGNTGSNAVVFGLIGLANSVAIYNA 842
 DB 832 VTAIVFVAGTSVPDTFASKAALADVYIADASIGNTGSNAVVFGLIGLANSVAIYNA 891
 QY 843 LOGOEHVASGLTASVTLFTFAFCISVLLYRRPHLGEGELGGRGKLAFTWLFVSL 902
 DB 892 ANGEQKVSFGLTASVTLFTFAFCISVLLYRRPHLGEGELGGRGKLAFTWLFVSL 951
 QY 903 WLLYLFATLEAVCYIKGF 921
 DB 952 WLLYLFATLEAVCYIKGF 970

RESULT 4

ID	NACLI_HUMAN	STANDARD:	PRT:	973 AA.
AC	P33418;	Q9UBJL8; Q9URX6; O95849; Q9UDN1; Q9UDN2;		
DT	01-OCT-1993	(Rel. 27, Created)		
DT	16-OCT-2001	(Rel. 40, Last sequence update)		
DT	15-JUN-2002	(Rel. 41, Last annotation update)		
DE	Sodium/calcium exchanger 1 precursor (Na(+)/Ca(2+)-exchange protein 1).			
GN	SLC8A1 OR NCX1 OR CNC.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
CC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A. (ISOFORM 1).			
RC	TISSUE=Heart;			
RX	MEDLINE=92262521; PubMed=1374913;			
RA	Komuro I., Wenninger K.E., Phillips K.D., Izumo S.;			
RT	"Molecular cloning and characterization of the human cardiac Na+/Ca2+			
RL	exchanger cDNA.";			
RN	Proc. Natl. Acad. Sci. U.S.A. 89:4769-4773.(1992).			
RP	[2]			
RX	SEQUENCE FROM N.A. (ISOFORMS 3 AND 7).			
RA	MEDLINE=21136211; PubMed=11241183;			
RT	Van Eylen F., Bollen A., Herchevelz A.;			
RL	"NCX1 Na/Ca exchanger splice variants in pancreatic islet cells.";			
RN	J. Endocrinol. 168:517-526(2001).			
RT	[3]			
RP	SEQUENCE FROM N.A. (ISOFORM 7).			
RA	Margolin N.J., Chen W., Wang Q., Kennedy B.G.;			
RT	"Na+/Ca2+ exchanger isoforms in cultured human retinal pigment			
RL	epithelium.";			
RN	Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases.			
RP	[4]			
RX	SEQUENCE OF 1-603 FROM N.A.			
RA	Kolling T., Stromatt C., Scronce D., Moody T.;			
RL	Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.			
RN	[5]			
RP	SEQUENCE OF 850-973 FROM N.A.			
RA	Kozlowicz A., Stoneking T., Hawkins M., Le T.;			
RL	Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.			
RN	[6]			
RP	SEQUENCE OF 459-681 FROM N.A. (ISOFORM 10).			
RA	Lundquist P., Lundgren T., Grtll-Linde A., Linde A.;			
RL	Submitted (DEC-1998) to the EMBL/GenBank/DBJ databases.			
CC	-1- FUNCTION: RAPIDLY TRANSPORTS CA2+ DURING EXCITATION-CONTRACTION COUPLING. CA(2+) IS EXTRUDED FROM THE CELL DURING RELAXATION SO AS TO PREVENT OVERLOADING OF INTRACELLULAR STORES.			
CC	-1- ENZYME REGULATION: BY ATP.			
CC	-1- SUBCELLULAR LOCATION: Integral membrane protein. Plasma membrane.			
CC	-1- ALTERNATIVE PRODUCTS: AT LEAST 4 ISOFORMS: 1/NACAL/NCX1.1 (SHOWN HERE). 3/NACA3/NCX1.3. 7/NAC17/NCX1.7 AND 10/NACA10/NCX1.10; ARE PRODUCED BY ALTERNATIVE SPLITTING.			
CC	-1- TISSUE SPECIFICITY: CARDIAC SARCOLEMA.			
CC	-----			
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CC	-----			
DR	EMBL; M91368; AAA35702.1; -			
DR	EMBL; AF108388; AAF08967.1; -			
DR	EMBL; AF108389; AAF08968.1; -			
DR	EMBL; AF128524; AAD26362.1; -			
DR	EMBL; AC007281; AAF19237.1; -			
DR	EMBL; AC007254; AAF19235.1; -			
DR	EMBL; AF115505; AAD17213.1; -			
PIR	PIR; S32815; S32815.			
GENE	GeneW: HGNC:11068; SLC8A1.			

[illegible]

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OY 179 FTIIGICVYIPDGETRIKIKHLVFEITAAWSIFATIMLILAVSPGVQWEGLLT 238
    ||| :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB 180 FTIILACVYVDPGERIKIKHLRVFVTAAWSIFATIMLILAVSPGVQWEGLLT 239
OY 239 FFFPVCVLLAWADKRLFYKTKMKKRYTKDKHRIIEGDPKGC--IEMDKMMNSH 295
    ||| :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB 240 FFFPVCVLLAWADKRLFYKTKMKKRYTKDKHRIIEGDPKGC--IEMDKMMNSH 299
OY 296 ----FLDGNLVPLEGKEVD----ESREMTIRILDKOKHPEKDLDOLVEMANYALSHOQ 348
    ||| :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB 300 VENEFLDGLAV-LEVDERDDDEBARREKMARILKELOKHPEKDLDOLVEMANYALSHOQ 358
OY 349 KSRAPYRIOTATRMGTAGNLIKHAQAQAKKASMSVETDPEE-DPISKVFEDPCSYOC 407
    ||| :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB 359 KSRAPYRIOTATRMGTAGNLIKHAQAQAKKASMSVETDPEE-DPISKVFEDPCSYOC 418
OY 408 LENCAGVLLTVYRKGGDKMTMYVDYKTEDGSANAGADYEFTGTVLKGPETOKEFSVG 467
    ||| :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB 419 LENCAGVLLTVYRKGGDKMTMYVDYKTEDGSANAGADYEFTGTVLKGPETOKEFSVG 478
OY 468 IIDDDEEEDHEFVSLVNRTEEDPEEGMPAIPNSLPLRAVLASPCVATVTLDDDD 527
    ||| :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB 479 IIDDDEEEDHEFVSLVNRTEEDPEEGMPAIPNSLPLRAVLASPCVATVTLDDDD 535
OY 528 HAGIFTECDTIVHSEISIGMEVKVLRISGANGTVIIPRTVEGTAKGGEDEEDTGYCL 587
    ||| :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB 536 HAGIFTECDTIVHSEISIGMEVKVLRISGANGTVIIPRTVEGTAKGGEDEEDTGYCL 595
OY 588 EKNEDTIVTIRKIVDEEYERQENFTALGEPKWMENG----- 627
    ||| :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB 596 EKNEDTIVTIRKIVDEEYERQENFTALGEPKWMENG----- 655
OY 628 -----ISDVTDRK--LJMEERAKRIAEKMGKRVLGHPKLEVI 663
    ||| :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB 656 EGOVPRKAKHABHPLSTVITADYDOKPLTSKEEBERKRAEGRPLGHTIKLEVI 715
OY 664 IESEYEKKTVDKLIKTNLALVNGTHSWRQFMEATVYSAAGDEDESGEERLPSCPD 723
    ||| :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB 716 IESEYEKKTVDKLIKTNLALVNGTHSWRQFMEATVYSAAGDEDESGEERLPSCPD 775
OY 724 YMHFLTVWKKVLFACVPRTVEYCHGACPAVSLITIGMLTAIIGDILASHFGCTIGKDSV 783
    ||| :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB 776 YMHFLTVWKKVLFACVPRTVEYCHGACPAVSLITIGMLTAIIGDILASHFGCTIGKDSV 835
OY 784 TAVVFAPGTSVDPFASAAALODVYADASTIGNVTSNAVNVFGIGLAMSAAATYML 843
    ||| :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB 836 TAVVFAPGTSVDPFASAAALODVYADASTIGNVTSNAVNVFGIGLAMSAAATYML 895
OY 844 OQOEHFVSAAGTIAFSVTLTIFAFVYICISVLYLRPRHPLGELGSPRGCKLATTWLFSIA 903
    ||| :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB 896 NBOQFVSPGTLAFSTVLTIFAFVYICISVLYLRPRHPLGELGSPRGCKLATTWLFSIA 955
OY 904 LYILFATLEAVCYIKGF 921
    ||| :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB 956 LYILFATLEAVCYIKGF 973

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RP SEQUENCE FROM N.A.
RC TISSUE-Heart;
RX MEDLINE-95078257; PubMed-7986817;
RA Tsuruya Y., Bersohn M.M., Li Z., Nicoll D.A., Phillips K.D.;
RT "Molecular cloning and functional expression of the guinea pig
RT Cardiac Na(+)-Ca2+ exchanger.";
RL Biochim. Biophys. Acta 1196:97-99(1994).
CC -1- FUNCTION: RAPIDLY TRANSPORTS CA2+ DURING EXCITATION-CONTRACTION
CC COUPLING. CA(2+) IS EXTRUDED FROM THE CELL DURING RELAXATION
CC SO AS TO PREVENT OVERLOADING OF INTRACELLULAR STORES.
CC -1- ENZYME REGULATION: BY ATP.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Plasma membrane.
CC -1- TISSUE SPECIFICITY: CARDIAC SARCOLEMMMA.
CC -----
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CC -----
CC EMBL: U04955; AA073904.1;
CC InterPro: IPR003644; Calx_beta.
CC InterPro: IPR004837; NaCa_Exemb.
CC InterPro: IPR004836; Na_Ca_Ex.
CC Pfam: PF01699; Na_Ca_Ex; 2.
CC Pfam: PF03160; Calx_beta; 2.
CC PRINTS: PR01259; NACEXCHNGR.
CC SMART: SM00237; Calx_beta; 2.
CC TIGRFAMs: TIGR00845; caca; 1.
CC Transport: Anticport; Calcium
CC Transmembrane; Glycoprotein;
CC Calmodulin-binding; Repeat.
CC SIGNAL 1 32
CC CHAIN 33 970
CC DOMAIN 33 71
CC TRANSMEM 72 93
CC DOMAIN 94 133
CC TRANSMEM 134 155
CC DOMAIN 156 167
CC TRANSMEM 168 188
CC DOMAIN 189 199
CC TRANSMEM 200 222
CC DOMAIN 223 225
CC TRANSMEM 226 249
CC DOMAIN 250 769
CC TRANSMEM 770 789
CC DOMAIN 790 796
CC TRANSMEM 820 821
CC TRANSMEM 822 840
CC DOMAIN 841 871
CC TRANSMEM 872 892
CC DOMAIN 893 903
CC TRANSMEM 904 924
CC TRANSMEM 925 941
CC TRANSMEM 942 958
CC DOMAIN 959 970
CC TRANSMEM 970 970
CC DOMAIN 251 270
CC TRANSMEM 270 270
CC REPEAT 407 478
CC REPEAT 407 478
CC REPEAT 539 609
CC REPEAT 839 875
CC DOMAIN 236 239
CC DOMAIN 689 692
CC DOMAIN 756 760
CC MOD_RES 389 389
CC CARBOHYD 41 41
CC CARBOHYD 157 157
CC CARBOHYD 866 866
CC SEQUENCE 970 AA; 108071 MW; 72D364CB8BD157739 CRC64;

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Query Match 71.6%; Score 3432.5; DB 1; Length 970;
 Best Local Similarity 68.7%; Pred. No. 5, 1e-218;
 Matches 672; Conservative 112; Mismatches 129; Indels 65; Gaps 11;

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OY 1 MAMLRQPLTSAFLH-FGLVTFVL-FLNGLRAEAGSGDPVSTGQNNESCGSDCKEYV 58
DB 1 MRLSLSPYSSIGFHLAMTLLISHVDHITAEET---EMVEBGNBTGCTGCTGYCKKV 56
OY 59 ILPIPPBPSPISGDKIARIYVFAVLIYFVGLVSTIADPFMASTIEYTSQERVTIKKN 118
DB 57 ILPIPPBPSPISGDKIARIYVFAVLIYFVGLVSTIADPFMASTIEYTSQERVTIKKN 116
OY 119 GETSTTTTIVNNEETVSNLTMALGSSAPILLSLIEVCHGFACDGLSGSTIYGAFAFM 178
DB 117 GETTTTIVNNEETVSNLTMALGSSAPILLSLIEVCHGFACDGLSGSTIYGAFAFM 176
OY 179 FTITIGCVVYVDGETRIKHLRVEFTIAMSIFAYIMLILAVFSPGVOMEGLTL 238
DB 177 FTITIALCVVYVDGETRIKHLRVEFTIAMSIFAYIMLILAVFSPGVOMEGLTL 236
OY 239 FEPPICVLLANVADRRLLEFYKYMKKYRDKHRIIEEGHPKC---IENDGKAMNSH 295
DB 237 FEPPICVVFAWADRRLLEFYKYMKKYRDKHRIIEEGHPKC---IENDGKAMNSH 296
OY 296 ---FLDGNLVPLEGEVD---ESRREMRILKDKOKHPEKDLQVEMANYALSHOO 348
DB 297 VENFLDGNLV-LEVEDERODDEAREMARILKELKOKHPEKDLQVEMANYALSHOO 355
OY 349 KRAFIYRIQATMTMGAGNILKHAQAOKKASSMSVHTDEPE-DEISKVEFDPSCSYOC 407
DB 356 KRAFAEYRIQATMTMGAGNILKHAQAOKKASSMSVHTDEPE-DEISKVEFDPSCSYOC 415
OY 408 LENCAGVILTVVRKGDMSKMTYVDKTEDSGANAGADEFEFEGTVYVLRPGCEQKRFSG 467
DB 416 LENCAGVILTVVRKGDMSKMTYVDKTEDSGANAGADEFEFEGTVYVLRPGCEQKRFSG 475
OY 468 IIDDIFEDDEHFVRLSNVRIEEOPEEGMPALFNSLPLRAVLASCVATVITLDD 527
DB 476 IIDDIFEDDEHFVRLSNVRIEEOPEEGMPALFNSLPLRAVLASCVATVITLDD 532
OY 528 HAGITFEEDDTIHVSESTVMEKVKLRTSGANGTVIVPRVEGAKGGEDFEDTYGEL 587
DB 533 HAGITFEEDDTIHVSESTVMEKVKLRTSGANGTVIVPRVEGAKGGEDFEDTYGEL 592
OY 588 EKNNETVITVTKIVDEEYERQENFIALGEPKMKENG----- 627
DB 593 EKNNETVITVTKIVDEEYERQENFIALGEPKMKENG----- 652
OY 628 -----ISDVTDRK--LTMEEEPKRIAEWKGKPVLGHPKLEYI 663
DB 653 YGQPVLRKYNHARDHPISTVITIADEYDKOPLTSEKEERKIAELGRPILGEBTKLEYI 712
OY 664 IEESTVEKTTVDKLIKKTALVGVTHSWRDQFMEATYVSAAGDEDEDESGERLPSCHD 723
DB 713 IEESTVEKTTVDKLIKKTALVGVTHSWRDQFMEATYVSAAGDEDEDESGERLPSCHD 772
OY 724 YMHHLTVYMKVLAFCVPTREYCHGACRAVSILLIIGMTALITIGLASFPCTIGAKDSV 783
DB 773 YMHHLTVYMKVLAFCVPTREYCHGACRAVSILLIIGMTALITIGLASFPCTIGAKDSV 832
OY 784 TAVVEVAFGSTVDFEASAKAALODVYADASIGNVTSNANVVFAGIGLAMSAAATYAML 843
DB 833 TAVVEVAFGSTVDFEASAKAALODVYADASIGNVTSNANVVFAGIGLAMSAAATYAML 892
OY 844 OGOEETHVASGLTAFSVTLFTTAFCISVLYLRPRPHLGELGPGRCGLATTWLFEVSLM 903
DB 893 NEOEKVSPGTLAFSVTLFTTAFCISVLYLRPRPHLGELGPGRCGLATTWLFEVSLM 952
OY 904 ILIYIPATLEAYCYIKGF 921
DB 953 LIYIPFSSLEAYCHIKGF 970

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RESULT 6
ID NC1_RAT STANDARD: PRT: 971 AA.
AC 001728;
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Sodium/calcium exchanger 1 precursor (Na(+)/Ca(2+)-exchange protein
DE 1).
GN SLC8A1 OR NCX1.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-Heart;
RX MEDLINE=93138118; PubMed=8422940;
RA Low M., Kasir J., Rahamimoff H.;
RT "Cloning of the rat heart Na(+)-Ca2+ exchanger and its functional
RT expression in HeLa cells."
RL FEBS Lett. 316:63-67(1993).
RN [2]
RP SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.
RC TISSUE-Brain;
RX MEDLINE=93202244; PubMed=8454039;
RA Furman I., Cook O., Kasir J., Rahamimoff H.;
RT "Cloning of two isoforms of the rat brain Na(+)-Ca2+ exchanger gene
RT and their functional expression in HeLa cells."
RN FEBS Lett. 319:105-109(1993).
RN [3]
RP SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.
RC STRAIN-Sprague-Dawley; TISSUE-Kidney cortex;
RX MEDLINE=94253030; PubMed=8195112;
RA Lee S.-L., Yu A.S.-L., Lytton J.;
RT "Tissue-specific expression of Na(+)-Ca2+ exchanger isoforms."
RL J. Biol. Chem. 269:14849-14852(1994).
RN [4]
RP TISSUE SPECIFICITY.
RC STRAIN-Sprague-Dawley;
RX MEDLINE=96394663; PubMed=8798769;
RA Nicoll D.A., Quednau B.D., Qui Z., Xia Y.-R., Lusis A.J.,
RA Philipson K.D.;
RT "Cloning of a third mammalian Na+-Ca2+ exchanger, NCX3."
RL J. Biol. Chem. 271:24914-24921(1996).
CC -1- FUNCTION: RAPIDLY TRANSPORTS CA2+ DURING EXCITATION-CONTRACTION
CC COUPLING. CA(2+) IS EXTRUDED FROM THE CELL DURING RELAXATION
CC SO AS TO PREVENT OVERLOADING OF INTRACELLULAR STORES.
CC -1- ENZYME REGULATION: BY ATP.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Plasma membrane.
CC -1- ALTERNATIVE PRODUCTS: 5 isoforms; heart/NCX1 (shown here),
CC brain 1/NCX5, brain 2/NCX4, kidney 1/NCX7 and kidney 2/NCX3;
CC are produced by alternative splicing.
CC -1- TISSUE SPECIFICITY: CARDIAC SARCOLEMA OR BRAIN, AND SPLEEN.
CC -----
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CC -----
DR EMBL: X68191; CAA48273.1; -
DR EMBL: X68812; CAA48707.1; -
DR EMBL: X68813; CAA48708.1; -
DR EMBL: U04933; AAB39952.1; -
DR EMBL: U04934; AAB19124.1; -
DR EMBL: U04936; AAA19125.1; -
DR PIR: S23552; S23552.
DR PIR: S28833; S28833.
DR InterPro: IPR003644; Calx_beta.
DR InterPro: IPR004837; Naca_Exmemb.

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DR	InterPro:IPR004836; Na_Ca_Ex.
DR	Pfam: PF01699; Na_Ca_Exp. 2.
DR	Pfam: PF03160; Calx-Beta. 2.
DR	PRINTS: PR01259; NACALCXCHNGR.
DR	TIGRFAMs: TIGR00845; Caca. 1.
KW	Transport; Antiport; Calcium transport; Sodium transport;
KM	Transmembrane; Glycoprotein; Phosphorylation; Signal;
KV	Calmodulin-binding; Repeat; Alternative splicing.
FT	SIGNAL 1 32 POTENTIAL.
FT	CHAIN 33 971 SODIUM/CALCIUM EXCHANGER 1.
FT	DOMAIN 33 71 EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM 72 93 POTENTIAL.
FT	DOMAIN 94 133 CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM 134 155 POTENTIAL.
FT	DOMAIN 156 167 EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM 168 188 POTENTIAL.
FT	DOMAIN 189 199 CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM 200 222 POTENTIAL.
FT	DOMAIN 223 225 EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM 226 249 POTENTIAL.
FT	DOMAIN 250 770 CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM 721 790 POTENTIAL.
FT	DOMAIN 791 797 EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM 798 820 POTENTIAL.
FT	DOMAIN 821 822 CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM 823 841 POTENTIAL.
FT	DOMAIN 842 872 EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM 873 893 POTENTIAL.
FT	DOMAIN 894 904 CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM 905 925 POTENTIAL.
FT	DOMAIN 926 942 EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM 943 959 POTENTIAL.
FT	DOMAIN 960 971 CYTOPLASMIC (POTENTIAL).
FT	DOMAIN 971 270 POLYUCLINIC-BINDING (BY SIMILARITY).
FT	REPEAT 138 178 ALPHA-1.
FT	REPEAT 407 478 BETA-1.
FT	REPEAT 539 609 BETA-2.
FT	REPEAT 840 876 ALPHA-2.
FT	DOMAIN 236 239 POLY-PHE.
FT	DOMAIN 690 693 POLY-GLU.
FT	DOMAIN 757 761 POLY-ASP.
FT	MOD_RES 389 389 PHOSPHORYLATION (BY SIMILARITY).
FT	CARBOHYD 411 441 N-LINKED (GLCNAC...) (POTENTIAL).
FT	CARBOHYD 157 157 N-LINKED (GLCNAC...) (POTENTIAL).
FT	CARBOHYD 867 867 N-DIMED (GLCNAC...) (POTENTIAL).
FT	VARSPLIC 602 635 TTTSKVIDDEEYKKETFEIIEGEPRLVMSEKK -> IITFIRDEEYEKCSFLVEPKTKRRGMK (IN KIDNEY ISOFORM 1 AND KIDNEY ISOFORM 2).
FT	VARSPLIC 636 642 MISSING (IN BRAIN ISOFORM 1, BRAIN ISOFORM 2, KIDNEY ISOFORM 1 AND KIDNEY ISOFORM 2).
FT	VARSPLIC 649 654 MISSING (IN BRAIN ISOFORM 1 AND KIDNEY ISOFORM 1).
FT	VARSPLIC 649 677 MISSING (IN BRAIN ISOFORM 2 AND KIDNEY ISOFORM 2).
FT	CONFLICT 250 250 D -> A (IN REF. 1).
FT	CONFLICT 402 402 P -> A (IN REF. 1).
FO	SEQUENCE 971 AA; 108184 MW; EC45GCEFAAF6A69 CRC64;

Query Match	71.5%	Score 3428;	DB 1;	Length 971;
Best Local Similarity	68.7%	Pred. No. 1e-217;		
Matches 675;	Conservative 106;	Mismatches 124;	Indels 78;	Gaps 11

Qy	4	LRLQELTALFHFQGLFVFLVLT-----	NGLEAEAGSGADVYSTGONNESCAGSDCK	55
Db	2	LRLSLPAPVSMGFRVLTVALLEFTHVDHITADTAEAGGN-----	ENTTECGSYCK	53
Qy	56	EGVILPIFYRPNPSPSGDKIARIVITYYPALAIYMFGLSVIINDRFMASTLEVIITSOERETIK	115	
Db	54	KGVILPIFPEPDPSPGDKIARIVITYYPAMVYMFGLSVIINDRFMASTLEVIITSOERETIK	113	
Qy	116	KPNCESTSTTITRVNVEVYSNLTJMALCGSSAPELLLSIEVCGHGFIAGDLPSTIVGSA	175	

Db	114	KPNSTGTTTVIRINNEYNSNLTLMAI	SSAPEILL	SVIEVGNHFTAGDGLSPSTYGSAA	173	
Qy	176	FNMFTIGICVYVIRPDGETRKIKLR	VPFTTAAMSIFA	YIMWILAVSPGVQWEG	235	
Db	174	FNMFTILACVYVDPDGETRKIKLR	VPFTTAAMSIFA	YIMWILAVSPGVQWEG	233	
Qy	236	LTLFFPACVLLAWAOKRLLFYUUM	KMKYATDKNRGIT	IIETBEDPHKG---	TIEMOKIM 2922	
Db	234	LTLFFPACVFAWADBRLLFTKTV	KTRKTRAGOKRMII	ENHESDRPASTETEMDSKV	293	
Qy	293	NSH---	FLDGNLVLPLEGKEND---	ESKRERIRILKDLKOKHPEKID	LDLOVEMANYALS 345	
Db	294	NSHVDNFTLDGALV-	LEVDERPDODEBARREMAR	ILTELKOKHPRDKIEQJL	IELANQVLS 3522	
Qy	346	HOOKSRAFYRIQATPMATGAGN	ILIKKHAEOAKKASSMEY	YHNDERE-DPISKVFDP	PCS 404	
Db	353	QOQKSRAFYRIQATPMLTGA	NIILKRHAADOKARAVSM	HEHNMVDVENDSVSKFFEGOT	412	
Qy	405	YOCLENGCAVLLTVYRKGD	SKMAYDYUKREDCSANA	AGADYETBETVYLKGEPOKEF	464	
Db	413	YOCLENGCTVALTLIRKGD	LJNLNPFVDEREDSTANA	GSYETBETVYLFKREPOKEI	472	
Qy	465	SVGIIDDDIFEDEHEFFRL	SNVRIIEEOPREPGMPAIF	NSLPLR-AVLASPCVATVI	523	
Db	473	RNGIIDDIFEDENEFVL	HSNVAVSSVSBDG---	ILDSNHSAIACGSPMTATIT	528	
Qy	534	LDDHAGJFTFECOTIHVSES	IGMEYKVLRTSGARCTV	YVPPFTVGTAKKGGEDEDT	563	
Db	529	FDDDHAGJFTFEEPRTHVSES	IGMEYKVLRTSGARNV	IIPYKTIEGTARGGGEDEDT	568	
Qy	564	YGELEFKNDENVKTRVY	IVDEEYERONEFIALGEP	KMKR-----	626	
Db	569	CGELEFONDELVKTVIS	AVDDIEYERKKKTFEIE	IGERPLWSEKALLNLN	LGCTLT 648	
Qy	627	-----	GISDVTDKR--	LTMEEERAKRIAEMGR	VPVLGEPH 658	
Db	649	BGCKMYGQRPVRKYNAR	HPRPSYVISISEEYD	KOPLTSKEEBERRIAEMGR	ILGRIEHT 708	
Qy	659	KLEVITIBESTYERKTTVD	KLKKTNALAVGTHS	KRDOPMEATIVYSAA	GDEDESGEERL 718	
Db	709	KLEVIIESEYERKSTVD	KLKKTNALAVGTHS	NRBOEIFAITYSAE	DDDDDECCEKEL 768	
Qy	719	PSCFPYVWHFLTVFKKVL	FACVCPREYCHGAC	PAVSLIIGMTLII	IGLASHFCTIG 778	
Db	769	PSCFPYVWHFLTVFKKVL	FACVCPREYCHGAC	PAVSLIIGMTLII	IGLASHFCTIG 828	
Qy	779	LKDSYTAJVAVFAFG	SVYDTPFASRAALOD	YVADASIGNVTGS	NAVNVFLGIGLANSVAA 838	
Db	829	LKDSYTAJVAVFALG	SVYDTPFASRAALOD	YVADASIGNVTGS	NAVNVFLGIGLANSVAA 888	
Qy	839	IYVALOGOEHFVSA	GLASFVLTFTIFAV	VCISVLLYRRRH	LOGELGGRGCKLATYWL 898	
Db	889	IYHANGNDQFVKS	POTLAFSVLTFTIF	AFINVGVALYRR	RREPEIGELGGRKAKLT	SSL 948
Qy	899	FVSLMLYITL	FATLEAYKIGF	921		
Db	949	FVSLMLYITL	FATLEAYKIGF	971		

RESULT 7			
ID	NACL_BOVIN	STANDARD:	PRT; 970 AA.
AC	P48765;		
DT	01-FEB-1996 (Rel. 33, Created)		
DT	01-FEB-1996 (Rel. 33, Last sequence update)		
DT	15-JUN-2002 (Rel. 41, Last annotation update)		
DE	Sodium/calcium exchanger 1 precursor (Na ⁺)/Ca ²⁺ -exchange protein		
DE	1).		
GN	SLC8A1.		
OS	Bos taurus (Bovine).		
OC	Eukaryota; Metazoa; Chordata; Craniala; Vertebrata; Euteleostomi;		
OC	Mammalia; Euteheria; Cetartiodactyla; Ruminantia; Pecora; Bovidea;		

OC Bovidae; Bovinae; Bos.
OX NCBI_Taxid=9913;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Heart;
RX MEDLINE=93037494; PubMed=1416984;
RA Aceto J.F., Condrescu M., Kroupis C., Nelson H., Nelson N.,
RT Nicoll D.A., Phillips K.D., Reeves J.P.;
RT "Cloning and expression of the bovine cardiac sodium-calcium
exchanger.";
RL Arch. Biochem. Biophys. 298:553-560(1992).
RN [2]
RP SUBCELLULAR LOCATION.
RC TISSUE=Retinal rod cell;
RX MEDLINE=90241959; PubMed=2334719;
RA Reid D.M., Friedel U., Moiday R.S., Cook N.J.;
RT "Identification of the sodium-calcium exchanger as the major
ricin-binding glycoprotein of bovine rod outer segments and its
localization to the plasma membrane.";
RL Biochemistry 29:1601-1607(1990).
CC -1- COUPLING. CA(2+) IS EXTRUDED FROM THE CELL DURING CONTRACTION
SO AS TO PREVENT OVERLOADING OF INTRACELLULAR STORES.
CC -1- ENZYME REGULATION: BY ATP.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Plasma membrane.
CC -1- TISSUE SPECIFICITY: CARDIAC SARCOLEMMMA.
CC -----
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entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
or send an email to license@isb-sib.ch).
CC -----
DR EMBL; L06438; AAA30509.1; -.
DR InterPro: IPR003644; Calx_beta.
DR InterPro: IPR004837; NaCa_Exmemb.
DR InterPro: IPR004836; Na_Ca_Ex.
DR Pfam: PF03160; NaCa_Ex; 2.
DR Pfam: PF03160; Calx_beta; 2.
DR PRINTS: PRO1259; NACAEXCHNGR.
DR SMART: SM00237; Calx_beta; 2.
DR TIGRFAMs: TIGR00845; caca; 1.
KW Transport: Antiport. Calcium transport; Sodium transport;
KW Transmembrane; Glycoprotein; Phosphorylation; Signal;
KW Calmodulin-binding; Repeat.
FT SIGNAL 1 32
FT CHAIN 33 970
FT DOMAIN 33 71
FT TRANSSEM 72 93
FT DOMAIN 94 133
FT TRANSSEM 134 135
FT DOMAIN 156 167
FT TRANSSEM 168 188
FT DOMAIN 189 199
FT TRANSSEM 200 222
FT DOMAIN 223 225
FT TRANSSEM 226 249
FT TRANSSEM 250 769
FT DOMAIN 770 789
FT TRANSSEM 790 796
FT TRANSSEM 797 819
FT DOMAIN 820 821
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FT DOMAIN 925 941
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FT DOMAIN 959 970
FT DOMAIN 251 270

FT REPEAT 138 178 ALPHA-1.
FT REPEAT 407 478 BETA-1.
FT REPEAT 539 609 BETA-2.
FT REPEAT 839 875 ALPHA-2.
FT DOMAIN 236 292 POLY-PHE.
FT DOMAIN 689 692 POLY-GLU.
FT DOMAIN 756 760 POLY-ASP.
FT MOD_RES 389 389 PHOSPHORYLATION (POTENTIAL).
FT CARBOHYD 41 41 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 157 157 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 866 866 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 970 AA; 108027 MW; 7C29153D1F87DBE CRC64;

Query Match 71.4%; Score 3425.5; DB 1; Length 970;
Best Local Similarity 68.7%; Pred. No. 1,56-217;
Matches 672; Conservative 110; Mismatches 131; Indels 65; Gaps 10;

1 MAMLRLOPLTSAFLHFGVTFVLV--LNLGRLEAGSGSDVPSGONNSCGSSDCKEGV 58
1 MQFSLSPFLSMGFVIAVMALFESHVDHISKFTMBEGNETGE---CTGSYCKKGV 56
59 ILPIWYENPSPSGDKIAKVIVYFVALIYFLGVSIIADRFMASEIVTSQEREVTIKRPN 118
57 ILPIWEPDPSFGDKIARATYFVAMVYMLGVSIIADRFMSISEVTSQEREVTIKRPN 116
119 GETSTTIRVNNETVSNLTIALMGSSAPEIIISLENGCHGIGIADLDSPSTVGSAAFTM 178
117 GETTIVIRVNNETVSNLTIALMGSSAPEIIISLENGCHGIGIADLDSPSTVGSAAFTM 176
179 FLIIGICVYVDPDGETRIRKILRVFFITFAASIFAYIMYLIAVFSFGVYQVWEGILTL 238
177 FLIILACVYVDPDGETRIRKILRVFFITFAASIFAYIMYLIIISVSSFGVYVWEGILTL 236
239 FFFPVCVLLAVNADKRLLPYKMKKRYTDKRGIIITEGDHPKG---IEMDKMAMNSH 295
237 FFFPVCVFAMVADKRLLPYKMKKRYTDKRGIIITEGDHPKG---IEMDKMAMNSH 296
296 ---FLDGNLVPLEKEVD---ESRREMIIRILDKOKNHPEDDOLVEMANYVALSHNQ 348
297 VDSFLDGNLV-LEVDRODDEAREREMARILKELKOKNHPEDDOLVEMANYVALSHNQ 355
349 KSRAFYRIQATRMNTGAGNIILKHAEOAKKASSSEVHTDEPE-DFTSKYFFDPCSYQC 407
356 KSRAFYRIQATRMNTGAGNIILKHAEOAKKASSSEVHTDEPE-DFTSKYFFDPCSYQC 415
408 LENCAGVILVYVRKGGDKNTWYVDYKTEDGSANAGADYEFTGTVVLKPGTQKEFSVG 467
416 LENCQVALLTIIRRGDGLTNVFDFTREDGANAGSDYEFTGTVVFKPGTQKEIRVG 475
468 IIDDIFEDDEHFVRLSNVRIEEOQREEGMPRAFFNSLPRLPRAVLASPCVATVITLDD 527
476 IIDDIFEDDEHFVRLSNVRIEEOQREEGMPRAFFNSLPRLPRAVLASPCVATVITLDD 532
528 HAGITFEPCDRIHVSSEISGVMEVKYLRTSGAGTYIVFPRVEGTAKGGEDFEDTGYEL 587
533 HAGITFEPCDRIHVSSEISGVMEVKYLRTSGAGTYIVFPRVEGTAKGGEDFEDTGYEL 592
588 EKKNDYKTIIRVKTIVDEEYERDEENFTALGEPKMERG----- 627
593 EFNQNDYKTIIRVKTIVDEEYERDEENFTALGEPKMERG----- 652
628 -----ISDVTDRK--LTMEDEEAKRIAMGKPVJGEMHKLVI 663
653 YGQPVFRVVAHREHPLSTITITIADEYDKOPLTSKEEERIRIAMGKPVJGEMHKLVI 712
664 IEESEYFTYVDKLIKTKTNLALVVGTHSMRQDFEATVYSAAGDEDESGEERTPSCFD 723
713 IEESEYFTYVDKLIKTKTNLALVVGTHSMRQDFEATVYSAAGDEDESGEERTPSCFD 772
724 YMHFLVFWKVLVFAVCPTEYCHGMAFVSIILIGMLTALIGDLASHFCCTIGLKDSY 783
773 YMHFLVFWKVLVFAVCPTEYCHGMAFVSIILIGMLTALIGDLASHFCCTIGLKDSY 832

QY 593 ETAKTRIVKIVDEEYERQENFFIALGEPKMERG----- 627
 DB 598 ELVKAKISKVIDDEYENKKNFFIEIGERPLVEMSEKALLNELGFTLTGKEMVGPDI 657
 QY 628 -----ISDVTDR--LTMEEEKAKRIEMKPVYGEHPKLEVTIEESY 668
 DB 658 FRKVAHDHPPIPTVITISEEDDKOPILSKSEERERIAEMGRPIIGETHTKEVITIOESY 717
 QY 669 EFKTVDKLIRKNTALVVGTHSRDQFMEATTVSAAGDEDESGEERTLPCFCFYVMEF 728
 DB 718 EFKSTVDKLIKNTALVVGTHSRDQFMEATTVSAAGDEDESGEERTLPCFCFYVMEF 777
 QY 729 LTVFKVYFACVPPTREYCHGNACFAVSIILIGMTAIGDLSHGCTIGLDSYAVAF 788
 DB 778 LTVFKVYFACVPPTREYCHGNACFAVSIILIGMTAIGDLSHGCTIGLDSYAVAF 837
 QY 789 VAFGTSVDPTEFASKAALQDVYADASIGNVTGSNAVNFGLIGLMSVAIYVALQGEF 848
 DB 838 VALGTSVDPTEFASKAALQDVYADASIGNVTGSNAVNFGLIGLMSVAIYVALQGEF 897
 QY 849 HVSAGTLAFSVTLFTIFAFVCSVLLYRRPHLGELGELGPRCKATITLPLFVLMILYTL 908
 DB 898 KVSPTGLAFSVTLFTIFAFVCSVLLYRRPHLGELGELGPRCKATITLPLFVLMILYTL 957
 QY 909 FATLAVCYIKGF 921
 DB 958 FSLSLATYCHIKGF 970

RESULT 9

ID NAC2_HUMAN STANDARD: PRT: 921 AA.
 AC Q9UPR5:

DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)

DE Sodium/calcium exchanger 2 precursor (Na(+)/Ca(2+)-exchange protein 2).

GN SLC8A2 OR NCX2 OR KIAA1087.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

OX NCBI_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=Brain;

RA MEDLINE=99397452; PubMed=10470851;

RA Kikuno R., Nagase T., Ishikawa K.-I., Hirose M., Miyajima N., Tanaka A., Kotani H., Nomura N., Ohara O.;

RA "Prediction of the coding sequences of unidentified human genes. XIV. The complete sequences of 100 new cDNA clones from brain which code for large proteins in vitro."

RL D-NA Res. 6:197-205(1999).

CC -1- FUNCTION: RAPIDLY TRANSPORTS CA2+ DURING EXCITATION-CONTRACTION COUPLING. CA(2+) IS EXTRUDED FROM THE CELL DURING RELAXATION SO AS TO PREVENT OVERLOADING OF INTRACELLULAR STORES (BY SIMILARITY).

CC -1- ENZYME REGULATION: BY ATP (BY SIMILARITY).

CC -1- SUBCELLULAR LOCATION: Integral membrane protein.

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CC EMBL; AB029010; BAA83039.1; ALT_INIT.

DR Genew; HGNC:11069; SLC8A2.

DR MIM; 601901;

DR InterPro; IPR003644; Calx_beta.
 DR InterPro; IPR004837; NacCa_Extmb.
 DR InterPro; IPR004836; Na_Ca_Ex.

DR Pfam; PF01699; Na_Ca_Ex; 2.
 DR Pfam; PF03160; Calx_beta; 2.
 DR PRINTS; PR01259; NACCAEXCHNR.
 DR SMART; SM00237; Calx_beta; 2.
 DR TIGRFAMs; TIGR00845; caca; 1.
 DR Transport; Antiport; Calcium
 KW Transmembrane; Glycoprotein;
 KW Calmodulin-binding; Repeat.
 FT SIGNAL 1 20
 FT CHAIN 21 921
 FT DOMAIN 21 68
 FT TRANSMEM 69 90
 FT DOMAIN 91 130
 FT TRANSMEM 131 152
 FT DOMAIN 153 164
 FT TRANSMEM 165 185
 FT DOMAIN 186 196
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 FT REPEAT 790 826
 FT DOMAIN 29 32
 FT DOMAIN 638 641
 FT CARBOHYD 34 34
 FT CARBOHYD 817 817
 SQ SEQUENCE 921 AA; 100367 MW; 798CCE7E32B9410C CRC64;

Query Match

Best Local Similarity 71.0%; Score 3373.5; DB 1; Length 921;

Matches 638; Conservative 124; Mismatches 104; Indels 33; Gaps 9;

QY 40 STGQNNSSGSSDCKEGYILPIWIPENSLDCKIARVYVVALYHPLGYSIIDRPM 99
 DB 39 STG---GGQGSYKQPGVLLPVWEPPDPSLDKARAVYVYVAMVYMLGVSIIDRPM 94
 QY 100 ASIEVTSOERVTIKKPPGETSTTIRVWNEVSNLTALMGSSAPETLSIEVCGHS 159
 DB 95 AIEVTSKEKETTITKANGETSQVTRVWNETVSNLTALMGSSAPETLSIEVCGHN 154
 QY 160 FTAGDLGPESTIGSAFNNFIIGICVYVDPGETRKIKHLRVFTTAAMSIFAYITLYM 219
 DB 155 FQAGELGPGTIVGSAFNNFVIAVCIVIPAGESKIKHLRVFTTASMSIFAYITLYM 214
 QY 220 ILAVSPGVQVWEGILTFEPFVVCVLLAVADKRLFLFKYMKKRTDKKHGIIETBG 279
 DB 215 ILAVSPGVQVWEGILTFEPFVVCVLLAVADKRLFLFKYMKKRTDKKHGIIETBG 274
 QY 280 DHPKGIEMDGKMNSHFDGNL----VLEKEVEDSRRIRILKDKOKHPKIDLPQ 334
 DB 275 DHPKGIEMDGKMNSHFDGNL----VLEKEVEDSRRIRILKDKOKHPKIDLPQ 333
 QY 335 LVEMANYVALSHQOKSRARYRQATRMVMTGAQNIILKHAEOAKKASMSSEVHTDEPDF 394
 DB 334 LVGIANYVALSHQOKSRARYRQATRMVMTGAQNIILKHAEOAKKASMSSEVHTDEPDF 392
 QY 395 ISKVFEPDPCSTOCLENGAVLTVYRKGGDMKTKMYVYKTTEDGSANAGADYEFTEGTVV 454


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Db 536 WNOQELWVKEQOLNRPVAKVVALGDLSPGDDTVVDEQDNKRLKLSMLTRG----- 651
Qy 300 NIVPLEGKVEDSRRR-MIRILKDKOKHPEKDLQ--LVEANYYALSHOOKSAFIRI 356
Db 652 SSASHNSTINSTIYQOLMLHSLDPGEGARPSKDKKEETLIPRAK----- 695
Qy 357 QATRMWTGAGNLIKHAQAQKASSMSFVHTDEP-----DETISKVFEDPCSYQC 407
Db 636 -----AIPQAKAESKPEEPRAKLEPEVITVPAPAPADVKGDDEDEGSGQV 739
Qy 408 ---LENGC-----AVLLTVVRKGDMSKTYVYDKTEDGS-----ANAGADYEFT 449
Db 740 GAEAENTERTGGEAEAPAECEGERSGDDALGEGSEKKAENESEGDIPARRDDE-D 798
Qy 450 EGTVVLKKGEGOKESVGI-----DDIFE-----EDEHFFPRLSNV 487
Db 799 EGEIAEGEYKVGDEDEEIQAGEGEGVDEDEEIQAGEGEGVDEDEEIQAGEG 858
Qy 488 RIEEORPE-----EGMPAIFNSLPRAVLASPCVAVTILDDHAGIFTEPC 536
Db 859 EYEGGDEDEEIQAGEGEGV-----DEDEGEIQAGEFA 891
Qy 537 DTIVHSESIGVMEKVLRTSGARGVIVPFTVEGTANG-----GEDFEDTYGELEFK 590
Db 892 GEVEGEDEGEIQ-----AGEGGEV-----KGDEGEIQAGEGVEGED-----GEVEGG 936
Qy 591 NDETUKTIRVKIVDEEYERQENFIALGEPKMERGI-----SVYTDKRLMEERE 642
Db 937 BDE--GEIQAGEGEGEGEQLNAEIQGEAKDDEGVDEGGGSGGGEDEDEE 994
Qy 643 AKRIEMGKPVLEGHPKLEVIIEESYEFKTYVDKLKIKTNLALVGTSHMRQFMEATV 702
Db 995 D-----EEEEE----- 1000
Qy 703 SAAGDEDESGEERLPSCFDY-----VHFLTVMKVLFACVPTTEYCHGNACAV 754
Db 1001 -----EEEEEEENQPLSLPEWPETRRKQAIYLFLLPIYFPLMLVPPDVRLEAKKFVI 1056
Qy 755 ----SILIIGMTALIIGLASHFGCTIGLKDSTAVNVAFSTVPDFASRAALQDVY 810
Db 1057 TFLGILMLIAMSFLYMLVMAHVOGETIGISEIMGILITLAICTSLPDLTISYIVARKGI- 1115
Qy 811 ADASIGNVTGSNAVNVFGLIGLAMSVAALYVALQGEFFHSAGTIAFSTVLTIFAFCI 870
Db 1116 GDMVASSVGSNIPTDITVGLPLPMLFSLINGLOPVAS-SNGLCALVLLFLLMFLVYS 1174
Qy 871 SVLYRRRPHUGELGEGPRCKLATTW-----LVYSMLLYTLF 909
Db 1175 SIATL-----CK-----WRMKILGFTMLFVYFV 1198

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RL Am. J. Physiol. 278:C651-C660(2000).
RN [2]
RP SEQUENCE OF 1067-1155 FROM N.A.
RA White K.E., Gesek F.A., Friedman P.A.;
RL Submitted (FEB-1996) to the EMBL/Genbank/DBJ databases.
CC -1- FUNCTION: Critical component of the visual transduction cascade,
CC controlling the calcium concentration of outer segments during
CC light and darkness. Light causes a rapid lowering of cytosolic
CC free calcium in the outer segment of both retinal rod and cone
CC photoreceptors and the light-induced lowering of calcium is caused
CC by extrusion via this protein which plays a key role in the
CC process of light adaptation. Transports one Ca(2+) and one K(+) in
CC exchange for four Na(+).
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- ALTERNATIVE PRODUCTS: 4 isoforms; 1 (shown here) 2, 3 and 4; are
CC produced by alternative splicing.
CC -1- TISSUE SPECIFICITY: Highly expressed in the eye.
CC -1- SIMILARITY: BELONGS TO THE SLC24A FAMILY OF TRANSPORTERS.
CC -----
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CC -----
DR EMBL, AF176688; AAD53121.1; -.
DR EMBL, U49235; AAB37753.1; -.
DR InterPro: IPR004817; K_NaCaexchang.
DR InterPro: IPR004481; K_NaCaexchng.
DR InterPro: IPR004837; NaCa_Extmemb.
DR Pfam, PF01699; Na_Ca_Ex_3.
DR TIGRFAMs, TIGR00367; K_NaCaexchang-rel; 1.
DR TIGRFAMs, TIGR00927; 2A1904; 1.
KW Vision; Transport; Antipport; Symport; Calcium transport;
KW Transmembrane; Glycoprotein; Phosphorylation; signal; Repeat;
KW Alternative splicing.
FT SIGNAL 1..38
FT CHAIN 39..1181
FT DOMAIN 39..419
FT TRANSMEM 420..440
FT DOMAIN 441..464
FT TRANSMEM 465..485
FT DOMAIN 486..491
FT TRANSMEM 492..512
FT DOMAIN 513..519
FT TRANSMEM 520..544
FT DOMAIN 545..552
FT TRANSMEM 553..569
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CC or send an email to license@slb-slb.ch).
CC -----
DR EMBL: AF062921: AAC16732.1: -
DR EMBL: AF062932: AAC72912.1: -
DR EMBL: AF026132: AAB7832.1: -
DR EMBL: AB014602: BAA31677.1: ALT_SEQ.
DR Genew: HGNC:10975: SLC24A1.
DR MIM: 603617: -
DR InterPro: IPR004817: K_NaCaexchang.
DR InterPro: IPR004837: NaCa_Exmemb.
DR InterPro: IPR004837: NaCa_Exmemb.
DR TIGRfams: TIGR00367: K_NaCaexchang-rel: 1.
DR TIGRfams: TIGR00927: 2A1904: 1.
DR Vision: Transport: Antiport; Symport; Calcium transport;
KW Transmembrane; Glycoprotein; Phosphorylation; Signal; Repeat;
KW Alternative splicing.
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FT SEQUENCE 1099 AA; 121374 MW; 3911856BB0885FD CRC64;

Query Match 6.1%; Score 293; DB 1; Length 1099;
Best Local Similarity 21.7%; Pred. No. 2.4e-11;
Matches 191; Conservative 122; Mismatches 268; Indels 298; Gaps 42;

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Db 614 -LSRRPVAKVMALEDL-----SKPGDAI-----AVDELQDNK---KLKPLSLLT----- 654
QY 368 ILKHAAGQAKASMSSEVHTDEPEDFISKVF---FDPCSYCLNCGAVILTVVRKGD 424
Db 655 -----RGSSSTSLHNSTIRSTIYQMLHSLDP-----LREVR----- 686
QY 425 MSKTVVDYKTEDEGSANAGADYEFTGTVLKPGELOKEFSVGIIDDIFFEEDEHFVRL 484
Db 687 LAK-----EKFEESLNGCARQ--PQAKAESR----- 712
QY 485 SNVRIEEDQPEEGMPAIFNSLPLRAVLASPCVATVITLDD--DHAGITFECDTHVS 542
Db 713 -----EEEBPAK-LPAVTVTPAPV-----DIKGDQKNBPG---GQEDVAEA 750
QY 543 ESIGVMEKVLRTSG-----ARGVIYVFRVEGTAGCGGDFPDYTGELFKND---E 593
Db 751 ESTGEMPEGEETAEGETEESKSGEETOPGEGETEOTGKEBCEDE--NEAGKGDNEGE 809
QY 594 TVKTRVKIVD-----EEERYOENFIALGEPKMMERGISD--VTDRKLMEEEKAKRIA 647
Db 810 DEGEIHAEDGEMKNGEGTESOELSAENHGEAKNDEKVEDGSGDGDSEEEEEEEO 869
QY 648 EMGKPEVLGEPKLEVIIEESYEFTKTVDKLIKTNLALVGTSHWRDQFMEAIVSAAD 707
Db 870 E-----EEEEEEQEEEE-----E 885
QY 708 EDEDSGEERLPSCFDY-----VMHFLYFMKVLVACVPPTCYCHMACFAY-----S 755
Db 886 EEEEEKGNDE-PLSLDWPETROKQAIYFLIPIVEPLMTVDPVROESRKEFFVTFLGS 944
QY 756 ILIIMTLAIIIDLSHSCCTIGLSDYAVAVFVAFGTSVPTPFASKAALADYVADASI 815
Db 945 IIMIMFSTLWMWMAHOVGETIGISEETIGLITLAGSIPPLTSVYARGL-GDMNV 1003
QY 816 GNVTSNANVAVLIGIGLAMSVAIYWALOGEYHVSAGTAFSVLFTFAFVCSIVLY 875
Db 1004 SSSVGSNIFDIVGLPVPPLFLSLNGLPVPS--SNGFCFAIVLLFLMLFVVISI--- 1059
QY 876 RRRPHLGELGPRCKCKATTW-----LFVSLMLYILF 909
Db 1060 -----ASCK-----WRMKNIIIGFTWELLYFVF 1081

RESULT 15
NCKX3_MOUSE STANDARD: PRT; 645 AA.
AC Q99PD7; Q99PD8; Q99JR2;.
DT 15-JUN-2002 (Rel. 41, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Sodium/potassium/calcium exchanger 3 precursor (Na(+)/K(+)/Ca(2+)-
exchange protein 3).
GN SLC24A3 OR NCKX3.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=129/SvJ, and CD-1; TISSUE=Embryonic stem cells, and Brain;
RA MEDLINE=21303617; PubMed=11294880;
RA Kraev A., Quednau B.D., Leach S., Li X.-F., Dong H., Winkfein R.,
RA Perizolo M., Cal X., Yang R., Phillips K.D., Lytton J.;
RT "Molecular cloning of a third member of the potassium-dependent
RT sodium-calcium exchanger gene family, NCKX3."
RL J. Biol. Chem. 276:23161-23172(2001).
RN [2]
RP SEQUENCE OF 323-645 FROM N.A.
RC TISSUE=Breast tumor;
RA Strausberg R.;
RL Submitted (Apr-2001) to the EMBL/GenBank/DBJ databases.
CC -I- FUNCTION: Transports one Ca(2+) and one K(+) in exchange for four
Na(+) (By similarity).
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CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- TISSUE SPECIFICITY: Abundant in the brain. Highest levels found in
CC selected thalamic nuclei, hippocampal CA1 neurons and in layer IV
CC of the cerebral cortex.
CC -1- SIMILARITY: BELONGS TO THE SLC24A FAMILY OF TRANSPORTERS.
CC -----
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CC -----
DR EMBL: AF314821; AAG60049.1; -.
DR EMBL: AF314822; AAG60050.1; -.
DR EMBL: BC005742; AAH05742.1; -.
DR MGI: 2137513; SLC24a3.
DR InterPro: IPR004481; K_NaCaexchng.
DR Pfam: PF01699; Na_Ca_Ex; 3.
DR Trifam: TRIGR00367; K_NaCaexchng-rel; 1.
KW Transport; Antiport; Symport; Calcium transport; Potassium transport;
KW Sodium transport; Transmembrane; Glycoprotein; Signal; Repeat.
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FT CHAIN 44 645 SODIUM/POTASSIUM/CALCIUM EXCHANGER 3.
FT DOMAIN 44 106 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 107 127 POTENTIAL.
FT DOMAIN 128 151 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 152 172 POTENTIAL.
FT DOMAIN 173 181 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 182 202 EXTRACELLULAR (POTENTIAL).
FT DOMAIN 203 209 CYTOPLASMIC (POTENTIAL).
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FT DOMAIN 231 234 EXTRACELLULAR (POTENTIAL).
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FT TRANSMEM 552 572 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 573 582 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 583 603 POTENTIAL.
FT DOMAIN 604 617 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 618 638 POTENTIAL.
FT DOMAIN 639 645 EXTRACELLULAR (POTENTIAL).
FT REPEAT 148 188 ALPHA-1.
FT REPEAT 188 520 ALPHA-2.
FT DOMAIN 424 430 POLY-GLU.
FT CARBOHYD 70 70 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 85 85 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT SEQUENCE 645 AA; 71914 MW; C62DB6CBA401C96 CRC64;

Query Match 5.5%; Score 266; DB 1; Length 645;
Best Local Similarity 19.1%; Pred. No. 6.6e-10;
Matches 162; Conservative 94; Mismatches 216; Indels 374; Gaps 30;

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QY 310 DESRREMRILKDKOKHPEKDLQVEMANYALSHQKSRFAFYRIOATRMGTAGNIL 369
|:|
DB 285 DDS----- 287
QY 370 KHAHAQAKKASSNSEVHDEPEDFISKVEFDPSCYOCLNCGAVLLTVYRKGDMSKTM 429
DB 288 ----- 294
QY 430 YDVKTEEDGSANAGADYEFTEGVTLKPGTQKEFSGIIDDFEEDHEFFRLSNVRI 489
DB 295 ----- 320
QY 490 EEEQPEEPMRAIFNSLPLRAVLASPCVATVTILDDHAGITFECDTIHVESIGVME 549
DB 321 QLSFSEAGLIMITSHRP-PKTRLS-MASMLINERORLINSRATYTGSEVAIKIP 375
QY 550 VKVLRISGARGTVIPRTVEGTAKGGGDEDEDYGELEFKNDETVKTIRKIVDEEYE 609
DB 376 IKHTVENGT-GPSAPDRGVNGTRR-DDIVAETD-----NETENE 413
QY 610 KOENFFIALGEPKMERGISDYVDKRLTMEEEAKRIAEGKRVLGEPKLEVIIESEY 669
DB 414 NEEN-----ENNEED-----EEEE----- 428
QY 670 FKTVDKLIKTNLALVGVTHSWRQFMEATVSAAGDEDEDE-----SGE-ERLP 719
DB 429 ----- 451
QY 720 SCFDYVNHFTLVFKVLFACVPTREYCHGV-----ACFAVSILIIIMLTAIGDLASHG 774
DB 452 WAFETWPLSF-----VLXFTVPNCNKP-WEKFWNTVFASSTLIMIAFSYMMVMWYIIG 504
QY 775 CTIGLDSVAVAVFAVFGTSVPDTPFASKAALODYVADASIGVNTGSNNVNVGLIGLAW 834
DB 505 YTLGIDPVILGITEFLAGTSVPCMASLIYARQGM-GDAVNSIGSNVFDILIGLGLPW 563
QY 835 SVAAI-----YVALOGSEFHVSAAGTLAFSV-----TLFTIFAF 867
DB 564 ALDTLAVDGSYIRLNSRGLITSVGLLASVFYTVGVHLNKWQDKKLGCGGLFLXGV 623
QY 868 VCISVL 873
DB 624 LCFSIM 629

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Search completed: November 30, 2002, 12:28:58
 Job time : 22.7346 secs